

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/934,367

DATE: 02/19/98
TIME: 11:13:37

INPUT SET: S23537.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#4

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Needleman, Philip
- 6 Glenn, Kevin
- 7
- 8 (ii) TITLE OF INVENTION: An Immunological Process and Constructs
- 9 for Increasing the HDL Cholesterol Concentration by DNA
- 10 Vaccination
- 11
- 12 (iii) NUMBER OF SEQUENCES: 52
- 13
- 14 (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Welsh & Katz, Ltd.
- 16 (B) STREET: 120 South Riverside Plaza, 22nd Floor
- 17 (C) CITY: Chicago
- 18 (D) STATE: IL
- 19 (E) COUNTRY: USA
- 20 (F) ZIP: 60606
- 21
- 22 (v) COMPUTER READABLE FORM:
- 23 (A) MEDIUM TYPE: Floppy disk
- 24 (B) COMPUTER: IBM PC compatible
- 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 27
- 28 (vi) CURRENT APPLICATION DATA:
- 29 (A) APPLICATION NUMBER:
- 30 (B) FILING DATE:
- 31 (C) CLASSIFICATION:
- 32
- 33 (viii) ATTORNEY/AGENT INFORMATION:
- 34 (A) NAME: Gamson Ph.D., Edward P.
- 35 (B) REGISTRATION NUMBER: 29,381
- 36 (C) REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
- 37
- 38 (ix) TELECOMMUNICATION INFORMATION:
- 39 (A) TELEPHONE: (312)655-1500
- 40 (B) TELEFAX: (312)655-1501
- 41
- 42
- 43 (2) INFORMATION FOR SEQ ID NO:1:
- 44
- 45 (i) SEQUENCE CHARACTERISTICS:
- 46 (A) LENGTH: 1431 base pairs

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47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: single
49 (D) TOPOLOGY: linear
50
51 (ii) MOLECULE TYPE: DNA (genomic)
52
53
54 (viii) POSITION IN GENOME:
55 (C) UNITS: bp
56
57
58 (x) PUBLICATION INFORMATION:
59 (A) AUTHORS: Drayna, Dennis
60 Jarnagin, Alisha Stephens
61 McLean, John
62 Henzel, William
63 Kohr, William
64 Fielding, Christopher
65 Lawn, Richard
66 (B) TITLE: Cloning and sequencing of human cholesteryl
67 ester transfer protein cDNA
68 (C) JOURNAL: Nature
69 (D) VOLUME: 327
70 (F) PAGES: 632-634
71 (G) DATE: June 18-1987
72
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
74
75 TGCTCCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA GCCTGCCCTC 60
76
77 CTGGTGTGTA ACCACGAGAC TGCCAAGGTC ATCCAGACCG CCTTCCAGCG AGCCAGCTAC 120
78
79 CCAGATATCA CGGGCGAGAA GGCCATGATG CTCCTTGGCC AAGTCAAGTA TGGGTGTCAC 180
80
81 AACATCCAGA TCAGCCACTT GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG 240
82
83 TCCATTGATG TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC 300
84
85 TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT CGACTCTGCC 360
86
87 ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG GTAGAGTGCG GACCGATGCC 420
88
89 CCTGACTGCT ACCTGTCTTT CCATAAGCTG CTCCTGCATC TCCAAGGGGA GCGAGAGCCT 480
90
91 GGGTGGATCA AGCAGCTGTT CACAAATTTT ATCTCCTTCA CCCTGAAGCT GGTCTTGAAG 540
92
93 GGACAGATCT GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA 600
94
95 AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT GACAGGTGAT 660
96
97 CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAGG GTCATTTTCAT CTACAAGAAT 720
98
99 GTCTCAGAGG ACCTCCCCCT CCCCACCTTC TCGCCACAC TGCTGGGGGA CTCCCGCATG 780

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100
101 CTGTACTTCT GGTTCCTCTGA GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT 840
102
103 GGCCGCCTCA TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC 900
104
105 TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTCGGCG GCTTCCCCAG CCAGGCCCAA 960
106
107 GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC AAAACAAGGG AGTCGTGGTC 1020
108
109 AATTCTTCAG TGATGGTGAA ATTCTCTTTT CCACGCCAG ACCAGCAACA TTCTGTAGCT 1080
110
111 TACACATTTG AAGAGGATAT CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC 1140
112
113 TTCTTAAGCC TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACCTT GACTGAGAGC 1200
114
115 AGCTCCGAGT CCATCCAGAG CTTCTCTCAG TCAATGATCA CCGCTGTGGG CATCCCTGAG 1260
116
117 GTCATGTCTC GGCTCGAGGT AGTGTTTTACA GCCCTCATGA ACAGCAAAGG CGTGAGCCTC 1320
118
119 TTCGACATCA TCAACCCTGA GATTATCACT CGAGATGGCT TCCTGCTGCT GCAGATGGAC 1380
120
121 TTTGGCTTCC CTGAGCACCT GCTGGTGGAT TTCCTCCAGA GCTTGAGCTA G 1431
122

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln
1 5 10 15

Val Ala Val His
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Ala Val Thr Phe Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
1 5 10 15Ala Tyr Arg Phe
20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp
1 5 10 15Phe Leu Gln Ser Leu Ser
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His Leu
1 5 10 15Leu Asp Phe Gln
20

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207 (2) INFORMATION FOR SEQ ID NO:6:

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209 (i) SEQUENCE CHARACTERISTICS:

210 (A) LENGTH: 20 amino acids

211 (B) TYPE: amino acid

212 (C) STRANDEDNESS: single

213 (D) TOPOLOGY: linear

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215 (ii) MOLECULE TYPE: peptide

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220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

221

222 Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Leu Lys Gln

223 1 5 10 15

224

225 Leu Phe Thr Asn

226 20

227

228 (2) INFORMATION FOR SEQ ID NO:7:

229

230 (i) SEQUENCE CHARACTERISTICS:

231 (A) LENGTH: 20 amino acids

232 (B) TYPE: amino acid

233 (C) STRANDEDNESS: single

234 (D) TOPOLOGY: linear

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236 (ii) MOLECULE TYPE: peptide

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241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

242

243 Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu Gly Arg Val Lys Tyr

244 1 5 10 15

245

246 Gly Leu His Asn

247 20

248

249 (2) INFORMATION FOR SEQ ID NO:8:

250

251 (i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 20 amino acids

253 (B) TYPE: amino acid

254 (C) STRANDEDNESS: single

255 (D) TOPOLOGY: linear

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257 (ii) MOLECULE TYPE: peptide

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SEQUENCE VERIFICATION REPORT
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Original Text